

Table IV. HLA Class I Standard Peptide Binding Affinity.

ALLELE	STANDARD PEPTIDE	SEQUENCE	SEQ ID NO:	STANDARD BINDING AFFINITY (nM)
A*0101	944.02	YLEPAIAKY	1189	25
A*0201	941.01	FLPSDYFPSV	1190	5.0
A*0202	941.01	FLPSDYFPSV	1191	4.3
A*0203	941.01	FLPSDYFPSV	1192	10
A*0205	941.01	FLPSDYFPSV	1193	4.3
A*0206	941.01	FLPSDYFPSV	1194	3.7
A*0207	941.01	FLPSDYFPSV	1195	23
A*6802	1072.34	YVIKVSARV	1196	8.0
A*0301	941.12	KVFPYALINK	1197	11
A*1101	940.06	AVDLYHFLK	1198	6.0
A*3101	941.12	KVFPYALINK	1199	18
A*3301	1083.02	STLPETYVRR	1200	29
A*6801	941.12	KVFPYALINK	1201	8.0
A*2402	979.02	AYIDNYNKF	1202	12
B*0702	1075.23	APRTLVL	1203	5.5
B*3501	1021.05	FPFKYAAAF	1204	7.2
B51	1021.05	FPFKYAAAF	1205	5.5
B*5301	1021.05	FPFKYAAAF	1206	9.3
B*5401	1021.05	FPFKYAAAF	1207	10

ay Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard Peptide	Sequence	SEQ ID NO:	Binding Affinity (nM)
DRB1*0101	DR1	515.01	PKYVKQNTLKLAT	1208	5.0
DRB1*0301	DR3	829.02	YKTIAFDEEARR	1209	300
DRB1*0401	DR4w4	515.01	PKYVKQNTLKLAT	1210	45
DRB1*0404	DR4w14	717.01	YARFQSQTTLKQKT	1211	50
DRB1*0405	DR4w15	717.01	YARFQSQTTLKQKT	1212	38
DRB1*0701	DR7	553.01	QYIKANSKFIGITE	1213	25
DRB1*0802	DR8w2	553.01	QYIKANSKFIGITE	1214	49
DRB1*0803	DR8w3	553.01	QYIKANSKFIGITE	1215	1600
DRB1*0901	DR9	553.01	QYIKANSKFIGITE	1216	75
DRB1*1101	DR5w11	553.01	QYIKANSKFIGITE	1217	20
DRB1*1201	DR5w12	1200.05	EALIHQLKINPYVLS	1218	298
DRB1*1302	DR6w19	650.22	QYIKANAKFIGITE	1219	3.5
DRB1*1501	DR2w2 $\beta$ 1	507.02	GRTQDENPVVHFFKNIVTP RTPPP	1220	9.1
DRB3*0101	DR52a	511	NGQIGNDPNRDIL	1221	470
DRB4*0101	DRw53	717.01	YARFQSQTTLKQKT	1222	58
DRB5*0101	DR2w2 $\beta$ 2	553.01	QYIKANSKFIGITE	1223	20

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

Table XIX p53 DR Super Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2wβ1	DR2w2β2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
VTCTYSPAL	1123	AKSVTCTYSPALNKM	1057	119								
LKDAQAGKE	1124	ALELKDAQAGKEPGG	1058	347								
VAPAPAPT	1125	APPVAPAPAPTAA	1059	70								
MPEAAPVA	1126	APRMPEAAPVAPAP	1060	63								
WPLSSVPS	1127	APSWPLSSSVPSQKT	1061	88								
IHYNYMCNS	1128	CTTIHYNYMCNSSCM	1062	229								
YFTLQIRGR	1129	DGEYFTLQIRGRERF	1063	324	0.0400			0.0150	-0.0027			
LSPDDIEQW	1130	DLMLSPDDIEQWTFE	1064	42								
VEPPLSQET	1131	DPSVEPPLSQETFS	1065	7				0.0039				
LRVEYLDDR	1132	EGNLRVEYLDDRNTF	1066	198								
VLSPLPSQA	1133	ENNVLSPLPSQAMDD	1067	28								
LAKTCPVQL	1134	FCQLAKTCPVQLWVD	1068	134								
LWKLLEN	1135	FSDLWKLLENVLS	1069	19								
LGFLHSGTA	1136	GFRLGFLHSGTAKSV	1070	108	1.9000	0.0360	0.1200	0.0027	8.3000	0.2000		
VRAMAIYKQ	1137	GTRVRAMAIYKQSQH	1071	154								
LPGSTKRA	1138	HHELPGSTKRALPN	1072	296								
VVPYEPPEV	1139	HSVVVPYEPPEVGSD	1073	214								
YMCNSSCMG	1140	HYNYMCNSSCMGGMN	1074	233								
WFTEDPGPD	1141	IEQWFTEDPGDEAP	1075	50	-0.0005				-0.0027			
LPNNTSSSP	1142	KRALPNNTSSSPQPK	1076	305								
LHSGTAKSV	1143	LGFLHSGTAKSVTCT	1077	111								
MFCQLAKTC	1144	LNMFCQLAKTCVQ	1078	130	0.2500	0.0016	0.0370	0.0006	0.0560	0.0080		
LPSQAMDDL	1145	LSPLPSQAMDDLMLS	1079	32								
ITLEDSSGN	1146	LTITLEDSSGNLLG	1080	252	-0.0005			0.0030	-0.0027			
MNRRPILTI	1147	MGMNRRPILTIITL	1081	243								
VVRRCPHHE	1148	MTEVVRRCPHHERCS	1082	169								
LELKDAQAG	1149	NEALELKDAQAGKEP	1083	345								
LSPLPSQAM	1150	NNVLSPLPSQAMDDL	1084	29								
IEQWFTEDP	1151	PDDIEQWFTEDPGPD	1085	47								
VGSDCTTIH	1152	PPEVGSDCCTTIHNY	1086	222				0.0380				
LWVDSTPPP	1153	PVQLWVDSTPPPPTGR	1087	142				0.0300				
VDSTPPPGT	1154	QLWVDSTPPPPTGRV	1088	144								
FLHSGTAKS	1155	RLGFLHSGTAKSVTC	1089	110								
FEVRVCACP	1156	RNSFEVRVCACPGRD	1090	267								
FRHSVVVPY	1157	RNTFRHSVVVPYEP	1091	209								
LTITILED	1158	RPILTITILEDSSGN	1092	249								
ILTIITLED	1159	RRPILTITILEDSSG	1093	248	0.0010				0.0100			
VRVCACPGR	1160	SFEVRVCACPGRDRR	1094	269								
LLGRNSFEV	1161	SGNLLGRNSFEVRVC	1095	261								
LNMFCQLA	1162	SPALNKMFCQLAKTC	1096	127								
MDDLMLSPD	1163	SQAMDDLMLSPDDIE	1097	37								
VPSQKTYQG	1164	SSSVPSQKTYQGSYG	1098	94								
VPEPPEVG	1165	SVVVPYEPPEVGSDC	1099	215				-0.0025				
LSSSVPSQK	1166	SWPLSSSVPSQKTYQ	1100	90								
FRLGFLHSG	1167	SYGFLGFLHSGTAK	1101	106								
LDDRNTFRH	1168	VEYLDDRNTFRHSVV	1102	203								
WVDSTPPPG	1169	VQLWVDSTPPPGTRV	1103	143								
YEPPEVGSD	1170	VVPYEPPEVGSDCTT	1104	217								
LPENNVLSP	1171	WKLLPENNVLSP	1105	23								
MCNSSCMGG	1172	YNYMCNSSCMGGMNR	1106	234								

as

AS  
Cont

Table XIX  
p53 DR Super Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
VTCTYSPAL	1123	AKSVTCTYSPALNKM	1057					
LKDAQAGKE	1124	ALELKDAQAGKEPGG	1058					
VAPAPAPT	1125	APPVAPAPAPTAA	1059					
MPEAAPVA	1126	APRMPEAAPVAPAP	1060					
WPLSSSVPS	1127	APSWPLSSSVPSQKT	1061					
IHYNYMCNS	1128	CTTIHYNYMCNSSCM	1062					
YFTLQIRGR	1129	DGEYFTLQIRGRERF	1063		-0.0018			
LSPDDIEQW	1130	DLMLSPDDIEQWFTE	1064					
VEPPLSQET	1131	DPSVEPPLSQETFS	1065					
LRVEYLDNR	1132	EGNLRVEYLDNRNIF	1066					
VLSPLPSQA	1133	ENNVLSPLPSQAMDD	1067					
LAKTCPVQL	1134	FCQLAKTCPVQLWVD	1068					
LWKLLPENN	1135	FSDLWKLLPENNVL	1069					
LGFLHSGTA	1136	GFRLGFLHSGTAKSV	1070	0.0460	0.2800	1.7000		
VRAMAIYKQ	1137	GTRVRAMAIYKQSQH	1071					
LPPGSTKRA	1138	HHELPPGSTKRALPN	1072					
VVPYEPPEV	1139	HSVVVPYEPPEVGSD	1073					
YMCNSSCMG	1140	HYNVYMCNSSCMGGMN	1074					
WFTEDPGPD	1141	IEQWFTEDPGPDEAP	1075		-0.0007			
LPNNTSSSP	1142	KRALPNNTSSSPQPK	1076					
LHSGTAKSV	1143	LGFLHSGTAKSVTCT	1077					
MFCQLAKTC	1144	LNMFCQLAKTCVPQ	1078	0.0096	0.1500	0.0320		
LPSQAMDDL	1145	LSPLPSQAMDDLMLS	1079					
ITLEDSSGN	1146	LTITLEDSSGNLLG	1080					
MNRRPILTI	1147	MGGMNRRLPILTIHL	1081		-0.0007			
VVRRCPHHE	1148	MTEVVRRCPHHERCS	1082					
LELKDAQAG	1149	NEALELKDAQAGKEP	1083					
LSPLPSQAM	1150	NNVLSPLPSQAMDDL	1084					
IEQWFTEDP	1151	PDDIEQWFTEDPGPD	1085					
VGSDCTTH	1152	PPEVGSDCTTHYNY	1086					
LWVDSTPPP	1153	PVQLWVDSTPPPGR	1087					
VDSTPPPGT	1154	QLWVDSTPPPGTRVR	1088					
FLHSGTAKS	1155	RLGFLHSGTAKSVTC	1089					
FEVRVCACP	1156	RNSFEVRVCACPGRD	1090					
FRHSVVVPY	1157	RNTFRHSVVVPYEPP	1091					
LTITLEDSS	1158	RPILTIITLEDSSGN	1092					
ILTIITLED	1159	RRPILTIITLEDSSG	1093		0.0023			
VRVCACPGR	1160	SFEVRVCACPGDRRR	1094					
LLGRNSFEV	1161	SGNLLGRNSFEVRVC	1095					
LNMFCQLA	1162	SPALNMFCQLAKTC	1096					
MDDLMLSPD	1163	SOAMDDLMLSPDDIE	1097					
VPSQKTYQG	1164	SSSVPSQKTYQGSYG	1098					
VPEPPEVG	1165	SVVVPYEPPEVGSDC	1099					
LSSSVPSQK	1166	SWPLSSSVPSQKTYQ	1100					
FRLGFLHSG	1167	SYGFRGFLHSGTAK	1101					
LDRNTFRH	1168	VEYLDNRNTFRHSVV	1102					
WVDSTPPPG	1169	VQLWVDSTPPPGTRV	1103					
YEPPEVGSD	1170	VVPYEPPEVGSDCTT	1104					
LPENNVLSP	1171	WKLLPENNVLSPPLPS	1105					
MCNSSCMGG	1172	YNYMCNSSCMGGMNR	1106					

AS  
cont.

Table XXa p53 DR 3a Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2w2B1	DR2w2B2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LSPDDIEQW	1173	DLMLSPDDIEQWFTE	1107	42				0.0150				
LRVEYLDLR	1174	EGNLRVEYLDLRNTF	1108	198				0.0039				
LSQETFSDL	1175	EPPLSQETFSDLWKL	1109	11				-0.0025				
FTEDPGPDE	1176	EQWFTEDPGPDEAPR	1110	51				-0.0025				
LDGEYFTLQ	1177	KKPLDGEYFTLQIRG	1111	320				-0.0025				
ITLEDSSGN	1178	LTITLEDSSGNLLG	1112	252				0.0030				
LLPENNVL	1179	LWKLLPENNVLSPPL	1113	22				0.0029				
VGSDCTTH	1180	PPEVGSDCTTHYNY	1114	222				0.0380				
LWVDSTPP	1181	PVQLWVDSTPPPGTR	1115	142				0.0300				
IRVEGNLRV	1182	QHLLRVEGNLRVEYL	1116	192				0.0960				
MFRELNEAL	1183	RFEMFRELNEALELK	1117	337				0.0052				
YLDNRNTR	1184	RVEYLDNRNTRHSV	1118	202				0.1800				
VPYEPPEVG	1185	SVVVPYEPPEVGSDC	1119	215				-0.0025				

AS  
conf.

p53 DR 3a Motif Peptides with Binding Data

Table XXa

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LSPDDIEQW	1173	DLMLSPDDIEQWFTE	1107					
LRVEYLDDR	1174	EGNLRVEYLDDRNTF	1108					
LSOETFSDL	1175	EPPLSQETFSDLWKL	1109					
FTEDPGPDE	1176	EQWFTEDPGPDEAPR	1110					
LDGEYFTLQ	1177	KKPLDGEYFTLQIRG	1111					
ITLEDSSGN	1178	LTITLEDSSGNLLG	1112					
LLPENNVL	1179	LWKLLPENNVLSPLP	1113					
VGSDCTTH	1180	PPEVGSDCTTHYNY	1114					
LWVDSPPPP	1181	PVQLWVDSPPPPGTR	1115					
IRVEGNLRV	1182	QHLRVEGNLRVEYL	1116					
MFRELNEAL	1183	RFEMFRELNEALELK	1117					
YLDNRNTFR	1184	RVEYLDNRNTFRHSV	1118					
VPYEPPEVG	1185	SVVVPYEPPEVGSDC	1119					

Table XXb p53 DR 3b Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2w2B1	DR2w2B2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
FTLQIRGRE	1186	GEYFTLQIRGRERFE	1120	325				0.0290				
VEGNLRVEY	1187	LIRVEGNLRVEYLDD	1121	194				0.0930				
YKQSQHMTE	1188	MAIYKQSQHMTEVVR	1122	160				-0.0025				

AS  
Conf

AS  
conclude

Table XXb p53 DR 3b Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
FTLQIRGRE	1186	GEYFTLQIRGRERFE	1120					
VEGNLRVEY	1187	LIRVEGNLRVEYLLDD	1121					
YKQSQHMT	1188	MAIYKQSQHMTVVVR	1122					



Table XXII. A2 supermotif analogs

Source	AA	Sequence	SEQ ID NO:	A*0201 nM
p53.24	9	KLLPENNVL	1224	313
p53.24V9	9	KLLPENNVV	1225	385
p53.25	11	LLPENNVLSPL	1226	19
p53.25V9	11	LLPENNVLSPV	1227	39
p53.65	9	RMPEAAPPV	1228	119
p53.65L2	9	RLPEAAPPV	1229	78
p53.65	10	RMPEAAPVA	1230	78
p53.65L2V10	10	RLPEAAPVV	1231	143
p53.65M2V10	10	RMPEAAPVV	1232	54
p53.69	8	AAPPVAPA	1233	5000
p53.69L2V8	8	ALPPVAPV	1234	217
p53.101	11	KTYQGSYGFR	1235	1786
p53.101L2V11	11	KLYQGSYGFRV	1236	81
p53.113	11	FLHSGTAKSVT	1237	5000
p53.113V11	11	FLHSGTAKSVV	1238	1220
p53.129	9	ALNKMFCQL	1239	735
p53.129V9	9	ALNKMFCQV	1240	75
p53.129B7V9	9	ALNKMFBQV	1241	192
p53.129	10	ALNKMFCQLA	1242	1316
p53.129V10	10	ALNKMFCQLV	1243	217
p53.132	9	KMFCQLAKT	1244	333
p53.132V9	9	KMFCQLAKV	1245	33
p53.132B4V9	9	KMFBQLAKV	1246	125
p53.132L2V9	9	KLFCQLAKV	1247	98
p53.135	9	CQLAKTCPV	1248	208
p53.135L2	9	CLLAKTCPV	1249	125
p53.135B1B7	9	BQLAKTBPV	1250	102
p53.135B1L2B7	9	BLLAKTBPV	1251	46
p53.139	9	KTCPVQLWV	1252	725
p53.139L2	9	KLCPVQLWV	1253	122
p53.139L2B3	9	KLBPVQLWV	1254	46
p53.149	9	STPPPGTRV	1255	909
p53.149M2	9	SMPPPGTRV	1256	172
p53.149L2	9	SLPPPGTRV	1257	122
p53.164	9	KQSQHMTEV	1258	500
p53.164L2	9	KLSQHMTEV	1259	122
p53.216	10	VVVPYEPPEV	1260	617
p53.216L2	10	VLVPYEPPEV	1261	89
p53.229	9	CTTIHYNM	1262	278
p53.229L2V9	9	CLTIHYNV	1263	263
p53.229B1L2V9	9	BLTIHYNV	1264	116
p53.236	8	YMCNSSCM	1265	4546
p53.236L2M8	8	YLCNSSCV	1266	--
p53.236	11	YMCNSSCMGGM	1267	667
p53.236L2M11	11	YLCNSSCMGGV	1268	22
p53.255	11	ITLEDSSGNLL	1269	1563
p53.255L2V11	11	ILLEDSSGNLV	1270	33
p53.256	10	TLEDSSGNLL	1271	1667
p53.256V10	10	TLEDSSGNLV	1272	4167

Table XXIIA A01 Analog Peptides

af

<u>Peptide</u>	<u>AA</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>	<u>Source</u>	<u>A*0101 nM</u>
52.0136	11	GSDCTTIHYN	1273	p53.226	67.6
57.0035	9	GTDCTTIHY	1274	p53.226.T2	0.9
57.0125	10	PTQKTYQGSY	1275	p53.98.T2	35.7
57.0126	10	GTDKSVTCTY	1276	p53.117.D3	42.4
57.0127	10	RVDGNLRVEY	1277	p53.196.D3	45.5

Cont

Al  
Conf

Table XXII B A03 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	A*0301 nM	A*1101 nM	A*3101 nM	A*3301 nM	A*6801 nM	A3 XRN
1371.14	10	KVYQGSYGFR	1278	p53.101.V2	37.9	61.9	72	10000	40	4
1371.15	10	KVYQGSYGFK	1279	p53.101.V2K10	33.3	9.2	138.5	-72500	38.1	4
1371.16	9	BVYSPALNK	1280	p53.124.B1V2	15.7	12.8	439	22307.7	500	4
1371.17	9	BVYSPALNR	1281	p53.124.B1V2R9	25	8.3	33.3	85.3	14.8	5
1371.18	8	KVFBQLAK	1282	p53.132.V2B4	846.2	461.5	7500	-72500	8888.9	1
1371.2	11	GVRVRAMAIYK	1283	p53.154.V2	57.9	136.4	418.6	-72500	13333.3	3
1371.22	9	RVRAMAIYR	1284	p53.156.R9	40.7	1666.7	8.6	138.1	666.7	3
1371.24	9	SVBMGGMNK	1285	p53.240.V2B3K9	12.5	17.1	9000	-72500	29.6	3
1371.25	10	SVBMGGMNRK	1286	p53.240.V2B3K10	100	75	-36000	-72500	17	3
1371.26	9	SVBMGGMNR	1287	p53.240.V2B3	161.8	95.2	120	852.9	11.1	4
1371.27	10	SVBMGGMNRR	1288	p53.240.V2B3	1000	25	620.7	805.6	11.4	2
1371.31	11	RVBABPGRDRK	1289	p53.273.B3B5K11	314.3	200	4615.4	-72500	2500	2
1371.32	11	SVSRHKKLMFK	1290	p53.376.V2	33.3	54.5	295.1	18125	1509.4	3
1371.33	11	SVSRHKKLMFR	1291	p53.376.V2R11	196.4	2857.1	183.7	1381	500	3


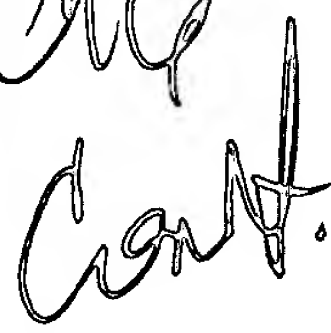

  


Table XXIIIC A02 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	A2 XRN
27.0068	9	KMFCQLAKT	1292	p53.132	505.1	14.3	19.6	92.5	-40000	3
39.0074	9	LLGRDSFEV	1293	mp53.261	41.7					
44.0003	9	LLGRDSFEV	1294	mp53.261	27.8					
1317.22	9	ALNKMFCQL	1295	p53.129	735.3	390.9	18.5	72.5	-80000	3
1317.23	9	KMFCQLAKT	1296	p53.132	333.3	33.1	17.5	105.7	-80000	4
1324.08	9	KQSQHMTVEV	1297	p53.164	500	130.3	169.5	284.6	-80000	4
1329.04	9	CTTIHYNM	1298	p53.229	277.8	286.7	2564.1	560.6	181.8	3
1329.07	9	KLLPENNVL	1299	p53.24	312.5	1954.5	12500	1193.5	-80000	1
1329.09	10	FLHSGTAKSV	1300	p53.113	357.1	179.2	14.5	4625	80000	3

Table XXIID A24 Analog Peptides



<u>Peptide</u>	<u>AA</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>	<u>Source</u>	<u>A*2401 nM</u>
52.008	8	TYQGSYGF	1301	p53.102	109.1
52.0081	8	SYGFRLGF	1302	p53.106	428.6
52.0103	10	TYQGSYGFRL	1303	p53.102	100
52.0104	10	TYSPALNKMF	1304	p53.125	2.4
52.0144	11	TYLWWVNNQSL	1305	CEA.353	46.2
52.0147	11	TYLWWVNGQSL	1306	CEA.531	92.3
57.0042	9	LYWVNGQSF	1307	CEA.533.Y2F9	15.8
57.0051	9	EYVNARHCF	1308	Her2/neu.553.F9	150
57.007	9	TYSDLWKLF	1309	p53.18.Y2F9	5.5
57.0071	9	SYGFRLGFF	1310	p53.106.F9	121.2
57.0096	10	TYQGSYGF RF	1311	p53.102.F10	30

AL  
Gand.

TABLE XXIIIE B07 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	B*0702 nM	B*3501 nM	B*5101 nM	B*5301 nM	B*5401 nM	B7 XRN
48.0055	8	FPALNKM	1312	p53.127.F1	0.025	3000	18333.3	6200	3846.2	1
48.0234	11	FPALNKMFCQL	1313	p53.127.F1	0.052	2482.8	5500	7750	500	2
48.0123	9	FPGTRVRAI	1314	p53.152.F1	1.1	-36000	662.7	23250	2439	1
48.0196	10	FPPGSTKRAL	1315	p53	0.79	-24000	6111.1	-23250	-20000	1
48.0127	9	FPQPKKKPI	1316	p53	0.61	-36000	-55000	-31000	16666.7	1
48.0128	9	FPQPKKKKPL	1317	p53	2.3	-36000	-55000	-31000	-100000	1

Table XXIII. Immunogenicity of A2 Supermotif Peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound	CTL Peptide <sup>1</sup>	CTL Wild-type	CTL Tumor
p53.135	9	CQLAKTCPV	1318	208	43.0	143.0	90.0	-- <sup>2</sup>	4		1/4	0/4
p53.69	8	AAPPVAPA	1319	5000	1536	1177	1233	4706	0			
p53.69L2V8	8	ALPPVAPV	1320	217	7167	500	285	67	4	2/4	1/3	0/3
p53.129	9	ALNKMFCQL	1321	735	391	19	73	-- <sup>2</sup>	3			
p53.129V9	9	ALNKMFCQV	1322	75	165	7.7	15	--	4	0/1		
p53.129B7V9	9	ALNKMFBQV	1323	192	391	23	49	--	4	2/4	0/3	0/2
p53.132	9	KMFCQLAKT	1324	333	33	18	106	--	4			
p53.132V9	9	KMFCQLAKV	1325	33	8.4	7.7	15	--	4	1/3	0/2	0/2
p53.132B4V9	9	KMFBQLAKV	1326	125	13	9.1	37	8889	4	5/5	0/4	0/4
p53.132L2V9	9	KLFCQLAKV	1327	98	3.6	3.4	9.5	1270	4	2/3	1/3	0/3
p53.139	9	KTCPVQLWV	1328	725	606	217	15	--	2			
p53.139L2	9	KLCPVQLWV	1329	122	239	29	23	--	4	2/5	2/3	1/3
p53.139L2B3	9	KLBPVQLWV	1330	45	29	19	31	--	4	3/4	2/3	1/2
p53.149	9	STPPPGTRV	1331	909	1162	1031	--	129	1			
p53.149L2	9	SLPPPGTRV	1332	122	226	13	9250	140	4	2/3	1/3	0/3
p53.149M2	9	SMPPPGTRV	1333	172	215	13	425	667	4	2/4	2/4	2/4
p53.216	10	VVVPYEPPEV	1334	617	1870	455	1194	--	1			
p53.216L2	10	VLVPYEPPEV	1335	89	391	71	2056	--	3	1/1	1/1	
p53.255	11	ITLEDSSGNLL	1336	1563	1265	2857	507	6667	0			
p53.255L2V11	11	ILLEDSSGNLV	1337	33	123	71	206	--	4	1/3	0/3	0/2

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity = 10,000nM.

Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

A. Class I binding assays			Radiolabeled peptide		SEQ ID NO:
Species	Antigen	Allele	Cell line	Source	
Human	A1	A*0101	Steinlin	Hu. J chain 102-110	YTAVVPLVY 1338
	A2	A*0201	JY	HBVc 18-27 F6->Y	FLPSDYFPSV 1339
	A2	A*0202	P815 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV 1340
	A2	A*0203	FUN	HBVc 18-27 F6->Y	FLPSDYFPSV 1341
	A2	A*0206	CLA	HBVc 18-27 F6->Y	FLPSDYFPSV 1342
	A2	A*0207	721.221 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV 1343
	A3		GM3107	non-natural (A3CON1)	KVFPYALINK 1344
	A11		BVR	non-natural (A3CON1)	KVFPYALINK 1345
	A24	A*2402	KAS116	non-natural (A24CON1)	AYIDNKNKF 1346
	A31	A*3101	SPACH	non-natural (A3CON1)	KVFPYALINK 1347
	A33	A*3301	LWAGS	non-natural (A3CON1)	KVFPYALINK 1348
	A28/68	A*6801	C1R	HBVc 141-151 T7->Y	STLPETYVVR 1349
	A28/68	A*6802	AMAI	HBV pol 646-654 C4->A	FTQAGYPAL 1350
	B7	B*0702	GM3107	A2 sigal seq. 5-13 (L7->Y)	APRTL VYLL 1351
	B8	B*0801	Steinlin	IVgp 586-593 Y1->F, Q5->	FLKDYQLL 1352
	B27	B*2705	LG2	R 60s	FRYNGLIHR 1353
	B35	B*3501	C1R, BVR	non-natural (B35CON2)	FPPKYAAAF 1354
	B35	B*3502	TISI	non-natural (B35CON2)	FPPKYAAAF 1355
	B35	B*3503	EHM	non-natural (B35CON2)	FPPKYAAAF 1356
	B44	B*4403	PITOUT	EF-1 G6->Y	AEMGKYSFY 1357
	B51		KAS116	non-natural (B35CON2)	FPPKYAAAF 1358
	B53	B*5301	AMAI	non-natural (B35CON2)	FPPKYAAAF 1359
	B54	B*5401	KT3	non-natural (B35CON2)	FPPKYAAAF 1360
	Cw4	Cw*0401	C1R	non-natural (C4CON1)	QYDDAVYKL 1361
	Cw6	Cw*0602	721.221 transfected	non-natural (C6CON1)	YRHDGGNVL 1362
	Cw7	Cw*0702	721.221 transfected	non-natural (C6CON1)	YRHDGGNVL 1363
Mouse	D <sup>b</sup>		EL4	Adenovirus E1A P7->Y	SGPSNTYPEI 1364
	K <sup>b</sup>		EL4	VSV NP 52-59	RGYVFQGL 1365
	D <sup>d</sup>		P815	HIV-IIIB ENV G4->Y	RGYRAFVTI 1366
	K <sup>d</sup>		P815	non-natural (KdCON1)	KFNPMKTYI 1367



Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

L <sup>d</sup>		P815	HBVs 28-39	IPQSLDSYWTSL	1368
B. Class II binding assays					
Species	Antigen	Allele	Cell line	Radiolabeled peptide	
				Source	Sequence SEQ ID NO:
Human	DR1	DRB1*0101	LG2	HA Y307-319	YPKYVVKQNTLKLAT 1369
	DR2	DRB1*1501	L466.1	MBP 88-102Y	VVHFFKNIVTPRTPPY 1370
	DR2	DRB1*1601	L242.5	non-natural (760.16)	YAAFAAAKTAATAFA 1371
	DR3	DRB1*0301	MAT	MT 65kD Y3-13	YKTIADFDEEAR 1372
	DR4w4	DRB1*0401	Preiss	non-natural (717.01)	YARFQSQTTLKQKT 1373
	DR4w10	DRB1*0402	YAR	non-natural (717.10)	YARFQRQTTLKAAA 1374
	DR4w14	DRB1*0404	BIN 40	non-natural (717.01)	YARFQSQTTLKQKT 1375
	DR4w15	DRB1*0405	KT3	non-natural (717.01)	YARFQSQTTLKQKT 1376
	DR7	DRB1*0701	Pitout	Tet. tox. 830-843	QYIKANSKFIGITE 1377
	DR8	DRB1*0802	OLL	Tet. tox. 830-843	QYIKANSKFIGITE 1378
	DR8	DRB1*0803	LUY	Tet. tox. 830-843	QYIKANSKFIGITE 1379
	DR9	DRB1*0901	HID	Tet. tox. 830-843	QYIKANSKFIGITE 1380
	DR11	DRB1*1101	Sweig	Tet. tox. 830-843	QYIKANSKFIGITE 1381
	DR12	DRB1*1201	Herluf	unknown eluted peptide	EALIHQLKINPYVLS 1382
	DR13	DRB1*1302	H0301	Tet. tox. 830-843 S->A	QYIKANAKFIGITE 1383
	DR51	DRB5*0101	GM3107 or L416.3	Tet. tox. 830-843	QYIKANAKFIGITE 1384
	DR51	DRB5*0201	L255.1	HA 307-319	PKYVVKQNTLKLAT 1385
	DR52	DRB3*0101	MAT	Tet. tox. 830-843	NGQIGNDPNRDIL 1386
	DR53	DRB4*0101	L257.6	non-natural (717.01)	YARFQSQTTLKQKT 1387
	DQ3.1	DQA1*0301/DQB1*030	PF	non-natural (ROIV)	YAHAAHAAHAAHAAHAA 1388
Mouse	IA <sup>b</sup>		DB27.4	non-natural (ROIV)	YAHAAHAAHAAHAAHAA 1389
	IA <sup>d</sup>		A20	non-natural (ROIV)	YAHAAHAAHAAHAAHAA 1390
	IA <sup>k</sup>		CH-12	HEL 46-61	YNTDGGSTDYQILQINSR 1391
	IA <sup>s</sup>		LS102.9	non-natural (ROIV)	YAHAAHAAHAAHAAHAA 1392
	IA <sup>u</sup>		91.7	non-natural (ROIV)	YAHAAHAAHAAHAAHAA 1393
	IE <sup>d</sup>		A20	Lambda repressor 12-26	YLEDARRKKAIYEKKK 1394
	IE <sup>k</sup>		CH-12	Lambda repressor 12-26	YLEDARRKKAIYEKKK 1395

Alf  
Conclude

Table XXVI. Crossbinding of A2 supermotif peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound
p53.24	9	KLLPENNVL	1396	313	1955	--	1194	--	1
p53.25	11	LLPENNVLSPL	1397	19	6.2	4.5	12	1702	4
p53.65	10	RMPEAAPPVA	1398	78	102	13	841	--	3
p53.65	9	RMPEAAPPV	1399	119	23	22	70	--	4
p53.113	10	FLHSGTAKSV	1400	357	179	15	4625	--	3
p53.132	9	KMFCQLAKT	1401	333	33	18	106	--	4
p53.135	9	CQLAKTCPV	1402	208	43	143	90	--	4
p53.136	8	QLAKTCPV	1403	455	--	100	2643	1067	2
p53.164	9	KQSQHMTEV	1404	500	130	170	285	--	4
p53.187	11	GLAPPQHLIRV	1405	79	39	11	55	--	4
p53.193	11	HLIRVEGNLRV	1406	385	1387	83	1194	1778	2
p53.229	9	CTTIHYNM	1407	278	287	2564	561	181	3
p53.263	10	NLLGRNSFEV	1408	217	--	2500	881	--	1
p53.264	9	LLGRNSFEV	1409	85	358	37	206	--	4

-- indicates binding affinity = 10,000nM.

A7  
Conf.

Table XXVII. Immunogenicity of A2 supermotif peptides

Source	Sequence	SEQ ID NO:		A*0201		A*0202		A*0203		A*0206		A*6802		No. A2 Alleles	CTL Wild-type	CTL Tumor
				nM	nM	nM	nM	nM	nM	nM	nM	nM	nM			
p53.135	CQLAKTCPV	1410	208	43	143	90	--	2	4	1/4	0/1					

1) Number of donors yielding a positive response/total tested.  
2) -- indicates binding affinity =10,000nM.

Table XXVIII. Crossbinding of A2 supermotif analogs

Source	AA	Sequence	SEQ ID		A*0201		A*0202		A*0203		A*0206		A*6802		No. A2 Alleles Crossbound
			NO:		nM		nM		nM		nM		nM		
p53.69	8	AAPPVAPA	1411		5000		1536		1177		1233		4706		0
p53.69L2V8	8	ALPPVAPV	1412		217		7167		500		285		67		4
p53.101	11	KTYQGSYGFR	1413		1786		896		--		514		615		0
p53.101L2V1	11	KLYQGSYGFRV	1414		81		48		24		116		--		4
p53.129	9	ALNKMFCQL	1415		735		391		19		73		--		3
p53.129V9	9	ALNKMFCQV	1416		75		165		7.7		15		--		4
p53.129B7V9	9	ALNKMFBQV	1417		192		391		23		49		--		4
p53.129	10	ALNKMFCQLA	1418		1316		1075		71		4625		--		1
p53.129V10	10	ALNKMFCQLV	1419		217		287		71		7400		--		3
p53.132	9	KMFCQLAKT	1420		333		33		18		106		--		4
p53.132V9	9	KMFCQLAKV	1421		33		8.4		7.7		15		--		4
p53.132B4V9	9	KMFBQLAKV	1422		125		13		9.1		37		8889		4
p53.132L2V9	9	KLFCQLAKV	1423		98		3.6		3.4		10		1270		4
p53.135	9	CQLAKTCPV	1424		208		43		143		90		--		4
p53.135L2	9	CLLAKTCPV	1425		125		506		67		370		--		3
p53.135B1B7	9	BQLAKTBPV	1426		102		71		15		67		--		4
p53.135B1L2I	9	BLLAKTBPV	1427		46		119		7.7		64		--		4
p53.139	9	KTCPVQLWV	1428		725		606		217		15		--		2
p53.139L2	9	KLCPVQLWV	1429		122		239		29		23		--		4
p53.139L2B3	9	KLBPVQLWV	1430		46		29		19		31		--		4
p53.149	9	STPPPGTRV	1431		909		1162		1031		--		129		1
p53.149M2	9	SMPPPGTRV	1432		172		215		13		425		667		4
p53.149L2	9	SLPPPGTRV	1433		122		226		13		9250		140		4
p53.164	9	KSQHMTVEV	1434		500		130		170		285		--		4
p53.164L2	9	KLSQHMTVEV	1435		122		94		35		46		--		4
p53.216	10	VVVPYEPPEV	1436		617		1870		455		1194		--		1
p53.216L2	10	VLVPYEPPEV	1437		89		391		71		2056		--		3
p53.236	11	YMCNSSCMGGM	1438		667		391		67		974		5333		2
p53.236L2M1	11	YLCNSSCMGGV	1439		22		13		3.6		18		1569		4
p53.255	11	ITLEDSSGNLL	1440		1563		1265		2857		507		6667		0
p53.255L2V1	11	ILLEDSSGNLV	1441		33		123		71		206		--		4

-- indicates binding affinity = 10,000nM.

Table XXIX. Immunogenicity of A2 supermotif analogs

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound	CTL Peptide <sup>1</sup>	CTL Wild-type	CTL Tumor
p53.69	8	AAPPVAPA	1442	5000	1536	1177	1233	4706	0			
p53.69L2V8	8	ALPPVAPV	1443	217	7167	500	285	67	4	2/4	1/3	0/3
p53.129	9	ALNKMFCQL	1444	735	391	19	73	-- <sup>2</sup>	3			
p53.129V9	9	ALNKMFCQV	1445	75	165	7.7	15	--	4	0/1		
p53.129B7V9	9	ALNKMFBQV	1446	192	391	23	49	--	4	2/4	0/3	0/2
p53.132	9	KMFCQLAKT	1447	333	33	18	106	--	4			
p53.132V9	9	KMFCQLAKV	1448	33	8.4	7.7	15	--	4	1/3	0/2	0/2
p53.132B4V9	9	KMFBQLAKV	1449	125	13	9.1	37	8889	4	5/5	0/4	0/4
p53.132L2V9	9	KLFCQLAKV	1450	98	3.6	3.4	9.5	1270	4	2/3	1/3	0/3
p53.139	9	KTCPVQLWV	1451	725	606	217	15	--	2			
p53.139L2	9	KLCPVQLWV	1452	122	239	29	23	--	4	2/5	2/3	1/3
p53.139L2B3	9	KLBPVQLWV	1453	45	29	19	31	--	4	3/4	2/3	1/2
p53.149	9	STPPPGTRV	1454	909	1162	1031	--	129	1			
p53.149L2	9	SLPPPGTRV	1455	122	226	13	9250	140	4	2/3	1/3	0/3
p53.149M2	9	SMPPPGTRV	1456	172	215	13	425	667	4	2/4	2/4	2/4
p53.216	10	VVVPYEPPEV	1457	617	1870	455	1194	--	1			
p53.216L2	10	VLVPYEPPEV	1458	89	391	71	2056	--	3	1/1	1/1	
p53.255	11	ITLEDSSGNLL	1459	1563	1265	2857	507	6667	0			
p53.255L2V11	11	ILLEDSSGNLV	1460	33	123	71	206	--	4	1/3	0/3	0/2

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity = 10,000nM.

Table XXX. DR supertype primary binding

A7  
Cont.

Peptide	DR147 Algo Sum	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR147 Cross- binding
39.0307	2	GFR LGFLHSGTAKSV	1461	P53.108	3	5.4	89	3
39.0308	2	LNKMFCQLAKTCPVC	1462	P53.130	20	804	167	3
39.0309	2	MGGMNRRPILTIITL	1463	P53.243	--	--	--	0
39.0310	2	RRPILTIITLEDSSG	1464	P53.248	5000	4500	--	0
39.0311	2	KRALPNNTSSSPQPK	1465	P53.305	--	--	--	0
39.0312	2	DGEYFTLQIRGRERF	1466	P53.324	125	--	--	1

-- indicates binding affinity =10,000nM.

A2  
Conf.

Table XXXI. DR supertype cross-binding

Peptide	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR2w2 $\beta$ 1 nM	DR2w2 $\beta$ 2 nM	DR6w1 9 nM	DR5w1 1 nM	DR8w2 nM	DR147 Binding	Broad Binding (5/8)
39.0307	GFRLGFLHSGTAKSV	1467	p53.108	2.6	5.4	89	253	167	76	100	29	3	8
39.0308	LNKMFQQLAKTCPV	1468	p53.130	20	804	167	5688	541	365	2500	1531	3	5

-- indicates binding affinity = 10,000nM.

Table XXXII. DR3 binding

Peptide	Sequence	SEQ ID NC	Source	DR3 nM
39.0409	EPPLSQETFSDLWKL	1469	p53.11	--
39.0410	LWKLLPENNVLSPLP	1470	p53.22	--
39.0411	DLMLSPDDIEQWFTE	1471	p53.42	--
39.0412	EQWFTEDPGPDEAPR	1472	p53.51	--
39.0413	PVQLWVDSTPPPGTR	1473	p53.142	--
39.0414	MAIYKQSQHMTVEVR	1474	p53.160	--
39.0415	QHLIRVEGNLRVEYL	1475	p53.192	3125
39.0416	LIRVEGNLRVEYLDD	1476	p53.194	3226
39.0417	EGNLRVEYLDDRNTF	1477	p53.198	--
39.0418	RVEYLDDRNTFRHSV	1478	p53.202	1667
39.0419	SVVVPYEPPEVGSDC	1479	p53.215	--
39.0420	PPEVGSDCTTIHYN	1480	p53.222	7895
39.0421	LTITLEDSSGNLLG	1481	p53.252	--
39.0422	KKPLDGEYFTLQIRG	1482	p53.320	--
39.0423	GEYFTLQIRGRERFE	1483	p53.325	--
39.0424	RFEMFRELNEALELK	1484	p53.337	--

-- indicates binding affinity =10,000nM.

Q17

Conf.



Table XXXIII. HTL candidate peptides

*Q7*  
*conclude*

Peptide	Sequence	SEQ ID NO:	DR1 nM	DR4w 4 nM	DR7 nM	DR3 nM	DR2w 2 $\beta$ 1 nM	DR2w 2 $\beta$ 2 nM	DR6w 1 9 nM	DR5w 1 1 nM	DR8w 2 nM	DR14 7 Bindin g	Broad Binding (5/8)	DR 3 Binder
39.0307	GFRLGFLHSGTAKSV	1485	2.6	5.4	89	--	253	167	76	100	29	3	8	0
39.0308	LNKMFCQLAKTCPVQ	1486	20	804	167	--	5688	541	365	2500	1531	3	5	0

-- indicates binding affinity = 10,000nM.

column added

Table IV. HLA Class I Standard Peptide Binding Affinity.

ALLELE	STANDARD PEPTIDE	SEQUENCE	SEQ ID NO:	STANDARD BINDING AFFINITY (nM)
A*0101	944.02	YLEPAIAKY	1189	25
A*0201	941.01	FLPSDYFPSV	1190	5.0
A*0202	941.01	FLPSDYFPSV	1191	4.3
A*0203	941.01	FLPSDYFPSV	1192	10
A*0205	941.01	FLPSDYFPSV	1193	4.3
A*0206	941.01	FLPSDYFPSV	1194	3.7
A*0207	941.01	FLPSDYFPSV	1195	23
A*6802	1072.34	YVIKVSARV	1196	8.0
A*0301	941.12	KVFPYALINK	1197	11
A*1101	940.06	AVDLYHFLK	1198	6.0
A*3101	941.12	KVFPYALINK	1199	18
A*3301	1083.02	STLPETYVRR	1200	29
A*6801	941.12	KVFPYALINK	1201	8.0
A*2402	979.02	AYIDNYNKF	1202	12
B*0702	1075.23	APRTLVL	1203	5.5
B*3501	1021.05	FPFKYAAAF	1204	7.2
B51	1021.05	FPFKYAAAF	1205	5.5
B*5301	1021.05	FPFKYAAAF	1206	9.3
B*5401	1021.05	FPFKYAAAF	1207	10

Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard Peptide	Sequence	SEQ ID NO:	Binding Affinity (nM)
DRB1*0101	DR1	515.01	PKYVKQNTLKLAT	1208	5.0
DRB1*0301	DR3	829.02	YKTIAFDEEARR	1209	300
DRB1*0401	DR4w4	515.01	PKYVKQNTLKLAT	1210	45
DRB1*0404	DR4w14	717.01	YARFQSQTTLKQKT	1211	50
DRB1*0405	DR4w15	717.01	YARFQSQTTLKQKT	1212	38
DRB1*0701	DR7	553.01	QYIKANSKFIGITE	1213	25
DRB1*0802	DR8w2	553.01	QYIKANSKFIGITE	1214	49
DRB1*0803	DR8w3	553.01	QYIKANSKFIGITE	1215	1600
DRB1*0901	DR9	553.01	QYIKANSKFIGITE	1216	75
DRB1*1101	DR5w11	553.01	QYIKANSKFIGITE	1217	20
DRB1*1201	DR5w12	1200.05	EALIHQLKINPYVLS	1218	298
DRB1*1302	DR6w19	650.22	QYIKANAKFIGITE	1219	3.5
DRB1*1501	DR2w2 $\beta$ 1	507.02	GRTQDENPVVHFFKNIVTP RTPPP	1220	9.1
DRB3*0101	DR52a	511	NGQIGNDPNRDIL	1221	470
DRB4*0101	DRw53	717.01	YARFQSQTTLKQKT	1222	58
DRB5*0101	DR2w2 $\beta$ 2	553.01	QYIKANSKFIGITE	1223	20

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

core column moved from 200 to 250

Table XIX p53 DR Super Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2wB1	DR2wB2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
VTCTYSPAL	1123	AKSVTCTYSPALNKM	1057	119								
LKDAQAGKE	1124	ALELKDAQAGKEPGG	1058	347								
VAPAPAPT	1125	APPVAPAPAPTAA	1059	70								
MPEAAPVA	1126	APRMPEAAPVAPAP	1060	63								
WPLSSVPS	1127	APSWPLSSVPSQKT	1061	88								
IHYNYMCNS	1128	CTTIHYNYMCNSSCM	1062	229								
YFTLQIRGR	1129	DGEYFTLQIRGRERF	1063	324	0.0400							
LSPDDIEQW	1130	DLMLSPDDIEQWTFE	1064	42				0.0150	-0.0027			
VEPPLSQET	1131	DPSVEPPLSQETFS	1065	7								
LRVEYLDNR	1132	EGNLRVEYLDNRNTF	1066	198				0.0039				
VLSPLPSQA	1133	ENNVLSPLPSQAMDD	1067	28								
LAKTCPVQL	1134	FCQLAKTCPVQLWVD	1068	134								
LWKLLPENN	1135	FSDLWKLLPENNVL	1069	19								
LGFLHSGTA	1136	GFRLGFLHSGTAKSV	1070	108	1.9000	0.0360	0.1200	0.0027	8.3000		0.2000	
VRAMAIYKQ	1137	GTRVRAMAIYKQSQH	1071	154								
LPPGSTKRA	1138	HHELPPGSTKRALPN	1072	296								
VVPYEPPEV	1139	HSVVVPYEPPEVGSD	1073	214								
YMCNSSCMG	1140	HYNYMCNSSCMGGMN	1074	233								
WFTEDPGPD	1141	IEQWFTEDPGPDEAP	1075	50								
LPNNTSSSP	1142	KRALPNNTSSSPQPK	1076	305	-0.0005				-0.0027			
LHSGTAKSV	1143	LGFLHSGTAKSVTCT	1077	111								
MFCQLAKTC	1144	LNMFCQLAKTCVPQ	1078	130	0.2500	0.0016	0.0370	0.0006	0.0560		0.0080	
LPSQAMDDL	1145	LSPLPSQAMDDLMLS	1079	32								
ITLEDSSGN	1146	LTIITLEDSSGNLLG	1080	252	-0.0005			0.0030	-0.0027			
MNRRPILTI	1147	MGGMNRRLPILTIITL	1081	243								
VVRRCPHHE	1148	MTEVVRRCPHHERCS	1082	169								
LELKDAQAG	1149	NEALELKDAQAGKEP	1083	345								
LSPLPSQAM	1150	NNVLSPLPSQAMDDL	1084	29								
IEQWFTEDP	1151	PDDIEQWFTEDPGPD	1085	47								
VGSDCTTIH	1152	PPEVGSDCTTIHNY	1086	222								
LWVDSTPPP	1153	PVQLWVDSTPPPGR	1087	142				0.0380				
VDSTPPPGT	1154	QLWVDSTPPPGTRVR	1088	144				0.0300				
FLHSGTAKS	1155	RLGFLHSGTAKSVTC	1089	110								
FEVRVCACP	1156	RNSFEVRVCACPRGD	1090	267								
FRHVVVPY	1157	RNTFRHVVVPYEP	1091	209								
LTIITLED	1158	RPILTIITLEDSSGN	1092	249								
ILTIITLED	1159	RRPILTIITLEDSSG	1093	248	0.0010				0.0100			
VRVCACPGR	1160	SFEVRVCACPGRDRR	1094	269								
LLGRNSFEV	1161	SGNLLGRNSFEVRVC	1095	261								
LNMFCQLA	1162	SPALNKMFCQLAKTC	1096	127								
MDDLMLSPD	1163	SOAMDDLMLSPDDIE	1097	37								
VPSQKTYQG	1164	SSSVPSQKTYQGSYG	1098	94								
VPEPPEVG	1165	SVVVPYEPPEVGSDC	1099	215								
LSSSVPSQK	1166	SWPLSSSVPSQKTYQ	1100	90				-0.0025				
FRGLFLHSG	1167	SYGFRGLFLHSGTAK	1101	106								
LDRNTFRH	1168	VEYLDNRNTFRHSVV	1102	203								
WVDSTPPPG	1169	VQLWVDSTPPPGTRV	1103	143								
YEPPEVGSD	1170	VVPYEPPEVGSDCTT	1104	217								
LPENNVLSP	1171	WKLLPENNVLSP	1105	23								
MCNSSCMGG	1172	YNYMCNSSCMGGMNR	1106	234								

column moved  
end position

added  
column

Table XIX  
p53 DR Super Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
VTCTYSPAL	1123	AKSVTCTYSPALNKM	1057					
LKDAQAGKE	1124	ALELKDAQAGKEPGG	1058					
VAPAPAPT	1125	APPVAPAPAPTAA	1059					
MPEAAPPA	1126	APRMPEAAPPAAP	1060					
WPLSSSVPS	1127	APSWPLSSSVPSQKT	1061					
IHYNYMCNS	1128	CTTHYNYMCNSSCM	1062					
YFTLQIRGR	1129	DGEYFTLQIRGRERF	1063		-0.0018			
LSPDDIEQW	1130	DLMLSPDDIEQWFTE	1064					
VEPPLSQET	1131	DPSVEPPLSQETFS	1065					
LRVEYLDLDR	1132	EGNLRVEYLDLDRNTF	1066					
VLSPPLSQA	1133	ENNVLSPLPSQAMDD	1067					
LAKTCPVQL	1134	FCQLAKTCPVQLWVD	1068					
LWKLLPENN	1135	FSDLWKLLPENNVL	1069					
LGFLHSGTA	1136	GFRLGFLHSGTAKSV	1070	0.0460	0.2800	1.7000		
VRAMAIYKQ	1137	GTRVRAMAIYKQSQH	1071					
LPPGSTKRA	1138	HHELPPGSTKRALPN	1072					
VVPYEPPEV	1139	HSVVPYEPPEVGSD	1073					
YMCNSSCMG	1140	HYNYMCNSSCMGGMN	1074					
WFTEDPGPD	1141	IEQWFTEDPGPDEAP	1075		-0.0007			
LPNNTSSSP	1142	KRALPNNTSSSPQPK	1076					
LHSGTAKSV	1143	LGFLHSGTAKSVTCT	1077					
MFCQLAKTC	1144	LNMFCQLAKTCPVQ	1078		0.1500	0.0320		
LPSQAMDDL	1145	LSPLPSQAMDDLMLS	1079	0.0096				
ITLEDSSGN	1146	LTIITLEDSSGNLLG	1080					
MNRRPILTI	1147	MGGMNRRLPILTIITL	1081		-0.0007			
VVRRCPHHE	1148	MTEVVRRCPHHERCS	1082					
LELKDAQAG	1149	NEALELKDAQAGKEP	1083					
LSPLPSQAM	1150	NNVLSPLPSQAMDDL	1084					
IEQWFTEDP	1151	PDDIEQWFTEDPGPD	1085					
VGSDCTIHH	1152	PPEVGSDDCTIHHYNY	1086					
LWVDSTPPP	1153	PVQLWVDSTPPPGTR	1087					
VDSTPPPGT	1154	QLWVDSTPPPGTRVR	1088					
FLHSGTAKS	1155	RLGFLHSGTAKSVTC	1089					
FEVRVCACP	1156	RNSFEVRVCACPGRD	1090					
FRHSVVVPY	1157	RNTFRHSVVVPYEP	1091					
LTIITLED	1158	RPILTIITLEDSSGN	1092					
ILTIITLED	1159	RRPILTIITLEDSSG	1093		0.0023			
VRVCACPGR	1160	SFEVRVCACPGRDRR	1094					
LLGRNSFEV	1161	SGNLLGRNSFEVRVC	1095					
LNMFCQLA	1162	SPALNMFCQLAKTC	1096					
MDDLMLSPD	1163	SQAMDDLMLSPDDIE	1097					
VPSQKTYQG	1164	SSSVPSQKTYQGSYG	1098					
VPEPPEVG	1165	SVVVPYEPPEVGSDC	1099					
LSSSVPSQK	1166	SWPLSSSVPSQKTYQ	1100					
FRLGFLHSG	1167	SYGFLGFLHSGTAK	1101					
LDDRNTFRH	1168	VEYLDLDRNTFRHSV	1102					
WVDSTPPPG	1169	VQLWVDSTPPPGTRV	1103					
YEPEVGSD	1170	VVPYEPPEVGSDCTT	1104					
LPENNVLSP	1171	WKLLPENNVLSP	1105					
MCNSSCMGG	1172	YNYMCNSSCMGGMNR	1106					

Table XXa p53 DR 3a Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2w2B1	DR2w2B2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LSPDDIEQW	1173	DLMLSPDDIEQWFTF	1107	42				0.0150				
LRVEYLDNR	1174	EGNLRVEYLDNRNTF	1108	198				0.0039				
LSQETFSDL	1175	EPPLSQETFSDLWKL	1109	11				-0.0025				
FTEDPGPDE	1176	EQWFTEDPGPDEAPR	1110	51				-0.0025				
LDGEYFTLQ	1177	KKPLDGEYFTLQIRG	1111	320				-0.0025				
ITLEDSSGN	1178	LTITLEDSSGNLLG	1112	252				0.0030				
LLPENNVL	1179	LWKLLPENNVLSPPL	1113	22				0.0029				
VGSDCTTH	1180	PPEVGSDCTTHYNY	1114	222				0.0380				
LWVDSTPP	1181	PVQLWVDSTPPPGTR	1115	142				0.0300				
IRVEGNLRV	1182	QHLRVEGNLRVEYL	1116	192				0.0960				
MFRELNEAL	1183	RFEMFRELNEALELK	1117	337				0.0052				
YLDNRNTR	1184	RVEYLDNRNTRHSV	1118	202				0.1800				
VPYEPPEVG	1185	SVVVPYEPPEVGSDC	1119	215				-0.0025				

Table XXa

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
LSPDDIEQW	1173	DLMLSPDDIEQWFTE	1107					
LRVEYLDNR	1174	EGNLRVEYLDNRNTF	1108					
LSOETFSDL	1175	EPPLSQETFSDDLWKL	1109					
FTEDPGPDE	1176	EQWFTEDPGPDEAPR	1110					
LDGEYFTLQ	1177	KKPLDGEYFTLQIRG	1111					
ITLEDSSGN	1178	LTITLEDSSGNLLG	1112					
LLPENNVL	1179	LWKLLPENNVLSPPL	1113					
VGSDCTTH	1180	PPEVGSDCTTHYNY	1114					
LWVDSTPP	1181	PVQLWVDSTPPGTR	1115					
IRVEGNLRV	1182	QHLIRVEGNLRVEYL	1116					
MFRELNEAL	1183	RFEMFRELNEALELK	1117					
YLDNRNTFR	1184	RVEYLDNRNTFRHSV	1118					
VPYEPPEVG	1185	SVVVPYEPPEVGSDC	1119					

columns 1, 2, 3, 4, 5, 6, 7, 8, 9

Table XXb p53 DR 3b Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2w2B1	DR2w2B2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
FTLQIRGRE	1186	GEYFTLQIRGRERFE	1120	325				0.0290				
VEGNLRVEY	1187	LIRVEGNLRVEYLDD	1121	194				0.0930				
YKQSQHMTE	1188	MAIYKQSQHMTTEVVR	1122	160				-0.0025				

3222  
 1186

0.0290  
 0.0930  
 -0.0025



Table XXb p53 DR 3b Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
FTLQIRGRE	1186	GEYFTLQIRGRERFE	1120					
VEGNLRVEY	1187	LIRVEGNLRVEYLDD	1121					
YKQSQHMT	1188	MAIYKQSQHMTTEVVR	1122					

*[Handwritten mark]*

*[Handwritten notes: "DR 3b", "W2", "DR 3b"]*

*[Handwritten notes: "FTLQIRGRE", "VEGNLRVEY", "YKQSQHMT"]*

Table XXII. A2 supermotif analogs

Source	AA	Sequence	SEQ ID NO:	A*0201 nM
p53.24	9	KLLPENNVL	1224	313
p53.24V9	9	KLLPENNVV	1225	385
p53.25	11	LLPENNVLSPL	1226	19
p53.25V9	11	LLPENNVLSPV	1227	39
p53.65	9	RMPEAAPPV	1228	119
p53.65L2	9	RLPEAAPPV	1229	78
p53.65	10	RMPEAAPVA	1230	78
p53.65L2V10	10	RLPEAAPVV	1231	143
p53.65M2V10	10	RMPEAAPVV	1232	54
p53.69	8	AAPPVAPA	1233	5000
p53.69L2V8	8	ALPPVAPV	1234	217
p53.101	11	KTYQGSYGFR	1235	1786
p53.101L2V11	11	KLYQGSYGFRV	1236	81
p53.113	11	FLHSGTAKSVT	1237	5000
p53.113V11	11	FLHSGTAKSVV	1238	1220
p53.129	9	ALNKMFCQL	1239	735
p53.129V9	9	ALNKMFCQV	1240	75
p53.129B7V9	9	ALNKMFBQV	1241	192
p53.129	10	ALNKMFCQLA	1242	1316
p53.129V10	10	ALNKMFCQLV	1243	217
p53.132	9	KMFCQLAKT	1244	333
p53.132V9	9	KMFCQLAKV	1245	33
p53.132B4V9	9	KMFBQLAKV	1246	125
p53.132L2V9	9	KLFCQLAKV	1247	98
p53.135	9	CQLAKTCPV	1248	208
p53.135L2	9	CLLAKTCPV	1249	125
p53.135B1B7	9	BQLAKTBPV	1250	102
p53.135B1L2B7	9	BLLAKTBPV	1251	46
p53.139	9	KTCPVQLWV	1252	725
p53.139L2	9	KLCPVQLWV	1253	122
p53.139L2B3	9	KLBPVQLWV	1254	46
p53.149	9	STPPPGTRV	1255	909
p53.149M2	9	SMPPPGTRV	1256	172
p53.149L2	9	SLPPPGTRV	1257	122
p53.164	9	KQSQHMTEV	1258	500
p53.164L2	9	KLSQHMTEV	1259	122
p53.216	10	VVVPYEPPEV	1260	617
p53.216L2	10	VLVPYEPPEV	1261	89
p53.229	9	CTTIHYNM	1262	278
p53.229L2V9	9	CLTIHYNV	1263	263
p53.229B1L2V9	9	BLTIHYNV	1264	116
p53.236	8	YMCNSSCM	1265	4546
p53.236L2M8	8	YLCNSSCV	1266	--
p53.236	11	YMCNSSCMGGM	1267	667
p53.236L2M11	11	YLCNSSCMGGV	1268	22
p53.255	11	ITLEDSSGNLL	1269	1563
p53.255L2V11	11	ILLEDSSGNLV	1270	33
p53.256	10	TLEDSSGNLL	1271	1667
p53.256V10	10	TLEDSSGNLV	1272	4167

Table XXIIA A01 Analog Peptides

<u>Peptide</u>	<u>AA</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>	<u>Source</u>	<u>A*0101 nM</u>
52.0136	11	GSDCTTIHYN	1273	p53.226	67.6
57.0035	9	GTDCTTIHY	1274	p53.226.T2	0.9
57.0125	10	PTQKTYQGSY	1275	p53.98.T2	35.7
57.0126	10	GTDKSVTCTY	1276	p53.117.D3	42.4
57.0127	10	RVDGNLRVEY	1277	p53.196.D3	45.5

Table XXII B A03 Analog Peptides

Peptide	AA	Sequence
1371.14	10	KVYQGSYGFR
1371.15	10	KVYQGSYGFK
1371.16	9	BVYSPALNK
1371.17	9	BVYSPALNR
1371.18	8	KVFBQLAK
1371.2	11	GVRVRAMAIYK
1371.22	9	RVRAMAIYR
1371.24	9	SVBMGGMNK
1371.25	10	SVBMGGMNRK
1371.26	9	SVBMGGMNR
1371.27	10	SVBMGGMNR
1371.31	11	RVBABPGRDRK
1371.32	11	SVSRHKKLMFK
1371.33	11	SVSRHKKLMFR

SEQ ID NO:	Source	A*0301 nM	A*1101 nM	A*3101 nM	A*3301 nM	A*6801 nM	A3 XRN
1278	p53.101.V2	37.9	61.9	72	10000	40	4
1279	p53.101.V2K10	33.3	9.2	138.5	-72500	38.1	4
1280	p53.124.B1V2	15.7	12.8	439	22307.7	500	4
1281	p53.124.B1V2R9	25	8.3	33.3	85.3	14.8	5
1282	p53.132.V2B4	846.2	461.5	7500	-72500	8888.9	1
1283	p53.154.V2	57.9	136.4	418.6	-72500	13333.3	3
1284	p53.156.R9	40.7	1666.7	8.6	138.1	666.7	3
1285	p53.240.V2B3K9	12.5	17.1	9000	-72500	29.6	3
1286	p53.240.V2B3K10	100	75	-36000	-72500	17	3
1287	p53.240.V2B3	161.8	95.2	120	852.9	11.1	4
1288	p53.240.V2B3	1000	25	620.7	805.6	11.4	2
1289	p53.273.B3B5K11	314.3	200	4615.4	-72500	2500	2
1290	p53.376.V2	33.3	54.5	295.1	18125	1509.4	3
1291	p53.376.V2R11	196.4	2857.1	183.7	1381	500	3

added  
claim A

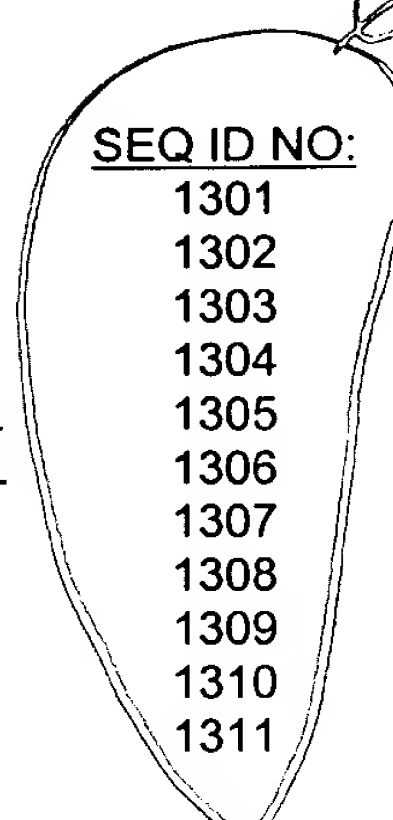
Table XXIIIC A02 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	A2 XRN
27.0068	9	KMFCQLAKT	1292	p53.132	505.1	14.3	19.6	92.5	-40000	3
39.0074	9	LLGRDSFEV	1293	mp53.261	41.7					
44.0003	9	LLGRDSFEV	1294	mp53.261	27.8					
1317.22	9	ALNKMFCQL	1295	p53.129	735.3	390.9	18.5	72.5	-80000	3
1317.23	9	KMFCQLAKT	1296	p53.132	333.3	33.1	17.5	105.7	-80000	4
1324.08	9	KQSQHMTVEV	1297	p53.164	500	130.3	169.5	284.6	-80000	4
1329.04	9	CTTIHYNM	1298	p53.229	277.8	286.7	2564.1	560.6	181.8	3
1329.07	9	KLLPENNVL	1299	p53.24	312.5	1954.5	12500	1193.5	-80000	1
1329.09	10	FLHSGTAKSV	1300	p53.113	357.1	179.2	14.5	4625	80000	3

*added column*

Table XXIID A24 Analog Peptides

<u>Peptide</u>	<u>AA</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>	<u>Source</u>	<u>A*2401 nM</u>
52.008	8	TYQGSYGF	1301	p53.102	109.1
52.0081	8	SYGFRLGF	1302	p53.106	428.6
52.0103	10	TYQGSYGFRL	1303	p53.102	100
52.0104	10	TYSPALNKMF	1304	p53.125	2.4
52.0144	11	TYLWWVNNQSL	1305	CEA.353	46.2
52.0147	11	TYLWWVNGQSL	1306	CEA.531	92.3
57.0042	9	LYWVNGQSF	1307	CEA.533.Y2F9	15.8
57.0051	9	EYVNARHCF	1308	Her2/neu.553.F9	150
57.007	9	TYSDLWKLF	1309	p53.18.Y2F9	5.5
57.0071	9	SYGFRLGFF	1310	p53.106.F9	121.2
57.0096	10	TYQGSYGFRF	1311	p53.102.F10	30



added to  
p53.102

TABLE XXIIE B07 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	B*0702 nM	B*3501 nM	B*5101 nM	B*5301 nM	B*5401 nM	B7 XRN
48.0055	8	FPALNKM	1312	p53.127.F1	0.025	3000	18333.3	6200	3846.2	1
48.0234	11	FPALNKMFCQL	1313	p53.127.F1	0.052	2482.8	5500	7750	500	2
48.0123	9	FPGTRVRAI	1314	p53.152.F1	1.1	-36000	662.7	23250	2439	1
48.0196	10	FPPGSTKRAL	1315	p53	0.79	-24000	6111.1	-23250	-20000	1
48.0127	9	FPQPKKKPI	1316	p53	0.61	-36000	-55000	-31000	16666.7	1
48.0128	9	FPQPKKKPL	1317	p53	2.3	-36000	-55000	-31000	-100000	1

added  
column

Table XXIII. Immunogenicity of A2 Supermotif Peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound	CTL Peptide <sup>1</sup>	CTL Wild-type	CTL Tumor
p53.135	9	CQLAKTCPV	1318	208	43.0	143.0	90.0	-- <sup>2</sup>	4		1/4	0/4
p53.69	8	AAPPVAPA	1319	5000	1536	1177	1233	4706	0			
p53.69L2V8	8	ALPPVAPV	1320	217	7167	500	285	67	4	2/4	1/3	0/3
p53.129	9	ALNKMFCQL	1321	735	391	19	73	-- <sup>2</sup>	3			
p53.129V9	9	ALNKMFCQV	1322	75	165	7.7	15	--	4	0/1		
p53.129B7V9	9	ALNKMFBQV	1323	192	391	23	49	--	4	2/4	0/3	0/2
p53.132	9	KMFCQLAKT	1324	333	33	18	106	--	4			
p53.132V9	9	KMFCQLAKV	1325	33	8.4	7.7	15	--	4	1/3	0/2	0/2
p53.132B4V9	9	KMFBQLAKV	1326	125	13	9.1	37	8889	4	5/5	0/4	0/4
p53.132L2V9	9	KLFCQLAKV	1327	98	3.6	3.4	9.5	1270	4	2/3	1/3	0/3
p53.139	9	KTCPVQLWV	1328	725	606	217	15	--	2			
p53.139L2	9	KLCPVQLWV	1329	122	239	29	23	--	4	2/5	2/3	1/3
p53.139L2B3	9	KLBPVQLWV	1330	45	29	19	31	--	4	3/4	2/3	1/2
p53.149	9	STPPPGTRV	1331	909	1162	1031	--	129	1			
p53.149L2	9	SLPPPGTRV	1332	122	226	13	9250	140	4	2/3	1/3	0/3
p53.149M2	9	SMPPPGTRV	1333	172	215	13	425	667	4	2/4	2/4	2/4
p53.216	10	VVVPYEPPEV	1334	617	1870	455	1194	--	1			
p53.216L2	10	VLVPYEPPEV	1335	89	391	71	2056	--	3	1/1	1/1	
p53.255	11	ITLEDSSGNLL	1336	1563	1265	2857	507	6667	0			
p53.255L2V11	11	ILLEDSSGNLV	1337	33	123	71	206	--	4	1/3	0/3	0/2

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity = 10,000nM.

*Handwritten signature and notes:*  
*10/10/01*  
*10/10/01*



Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

A. Class I binding assays					
Species	Antigen	Allele	Cell line	Radiolabeled peptide	
				Source	Sequence
Human	A1	A*0101	Steinlin	Hu. J chain 102-110	YTAVVPLVY
	A2	A*0201	JY	HBVc 18-27 F6->Y	FLPSDYFSPV
	A2	A*0202	P815 (transfected)	HBVc 18-27 F6->Y	FLPSDYFSPV
	A2	A*0203	FUN	HBVc 18-27 F6->Y	FLPSDYFSPV
	A2	A*0206	CLA	HBVc 18-27 F6->Y	FLPSDYFSPV
	A2	A*0207	'21.221 (transfected)	HBVc 18-27 F6->Y	FLPSDYFSPV
	A3		GM3107	non-natural (A3CON1)	KVFPYALINK
	A11		BVR	non-natural (A3CON1)	KVFPYALINK
	A24	A*2402	KAS116	non-natural (A24CON1)	AYIDNYNKF
	A31	A*3101	SPACH	non-natural (A3CON1)	KVFPYALINK
	A33	A*3301	LWAGS	non-natural (A3CON1)	KVFPYALINK
	A28/68	A*6801	C1R	HBVc 141-151 T7->Y	STLPETYVVR
	A28/68	A*6802	AMAI	HBV pol 646-654 C4->A	FTQAGYPAL
	B7	B*0702	GM3107	A2 sigal seq. 5-13 (L7->Y)	APRTL VYLL
	B8	B*0801	Steinlin	IVgp 586-593 Y1->F, Q5->	FLKDYQLL
	B27	B*2705	LG2	R 60s	FRYNGLIHR
	B35	B*3501	C1R, BVR	non-natural (B35CON2)	FPFKYAAAF
	B35	B*3502	TISI	non-natural (B35CON2)	FPFKYAAAF
	B35	B*3503	EHM	non-natural (B35CON2)	FPFKYAAAF
	B44	B*4403	PITOUT	EF-1 G6->Y	AEMGKYSFY
	B51		KAS116	non-natural (B35CON2)	FPFKYAAAF
	B53	B*5301	AMAI	non-natural (B35CON2)	FPFKYAAAF
	B54	B*5401	KT3	non-natural (B35CON2)	FPFKYAAAF
	Cw4	Cw*0401	C1R	non-natural (C4CON1)	QYDDA VYKL
	Cw6	Cw*0602	721.221 transfected	non-natural (C6CON1)	YRHDGGNVL
	Cw7	Cw*0702	721.221 transfected	non-natural (C6CON1)	YRHDGGNVL
Mouse	D <sup>b</sup>		EL4	Adenovirus E1A P7->Y	SGPSNTYPEI
	K <sup>b</sup>		EL4	VSV NP 52-59	RGYVVFQGL
	D <sup>d</sup>		P815	HIV-IIIB ENV G4->Y	RGPYRAFTI
	K <sup>d</sup>		P815	non-natural (KdCON1)	KFNPMKTYI

Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

L <sup>d</sup>		P815	HBVs 28-39	IPQSLDSYWTSL	1368
B. Class II binding assays					
Species	Antigen	Allele	Cell line	Radiolabeled peptide	
				Source	Sequence
Human	DR1	DRB1*0101	LG2	HA Y307-319	YPKYVKQNTLKLAT
	DR2	DRB1*1501	L466.1	MBP 88-102Y	VVHFFKNIVTPRTPPY
	DR2	DRB1*1601	L242.5	non-natural (760.16)	YAAFAAAKTAFAAFA
	DR3	DRB1*0301	MAT	MT 65kD Y3-13	YKTIAFDEEARR
	DR4w4	DRB1*0401	Preiss	non-natural (717.01)	YARFQSQTTLKQKT
	DR4w10	DRB1*0402	YAR	non-natural (717.10)	YARFQRQTTLKAAA
	DR4w14	DRB1*0404	BIN 40	non-natural (717.01)	YARFQSQTTLKQKT
	DR4w15	DRB1*0405	KT3	non-natural (717.01)	YARFQSQTTLKQKT
	DR7	DRB1*0701	Pitout	Tet. tox. 830-843	QYIKANSKFIGITE
	DR8	DRB1*0802	OLL	Tet. tox. 830-843	QYIKANSKFIGITE
	DR8	DRB1*0803	LUY	Tet. tox. 830-843	QYIKANSKFIGITE
	DR9	DRB1*0901	HID	Tet. tox. 830-843	QYIKANSKFIGITE
	DR11	DRB1*1101	Sweig	Tet. tox. 830-843	QYIKANSKFIGITE
	DR12	DRB1*1201	Herluf	unknown eluted peptide	EALIHQLKINPYVLS
	DR13	DRB1*1302	H0301	Tet. tox. 830-843 S->A	QYIKANAKFIGITE
	DR51	DRB5*0101	GM3107 or L416.3	Tet. tox. 830-843	QYIKANAKFIGITE
	DR51	DRB5*0201	L255.1	HA 307-319	PKYVVKQNTLKLAT
	DR52	DRB3*0101	MAT	Tet. tox. 830-843	NGQIGNDPNRDIL
	DR53	DRB4*0101	L257.6	non-natural (717.01)	YARFQSQTTLKQKT
	DQ3.1	QA1*0301/DQB1*030	PF	non-natural (ROIV)	YAHAAHAAHAAHAAHAA
Mouse	IA <sup>b</sup>		DB27.4	non-natural (ROIV)	YAHAAHAAHAAHAAHAA
	IA <sup>d</sup>		A20	non-natural (ROIV)	YAHAAHAAHAAHAAHAA
	IA <sup>k</sup>		CH-12	HEL 46-61	YNTDGGSTDYGILQINSR
	IA <sup>s</sup>		LS102.9	non-natural (ROIV)	YAHAAHAAHAAHAAHAA
	IA <sup>u</sup>		91.7	non-natural (ROIV)	YAHAAHAAHAAHAAHAA
	IE <sup>d</sup>		A20	Lambda repressor 12-26	YLEDARRKKAIYEKKK
	IE <sup>k</sup>		CH-12	Lambda repressor 12-26	YLEDARRKKAIYEKKK

-- indicates binding affinity = 10,000nM.

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles	Crossbound
p53.24	9	KLLPENNVL	1396	313	1955	--	1194	--	1	
p53.25	11	LLPENNVLSPL	1397	19	6.2	4.5	12	1702	4	
p53.65	10	RMPEAAPVVA	1398	78	102	13	841	--	3	
p53.65	9	RMPEAAPPV	1399	119	23	22	70	--	4	
p53.113	10	FLHSGTAKSV	1400	357	179	15	4625	--	3	
p53.132	9	KMFCQLAKT	1401	333	33	18	106	--	4	
p53.135	9	CQLAKTCPV	1402	208	43	143	90	--	4	
p53.136	8	QLAKTCPV	1403	455	--	100	2643	1067	2	
p53.164	9	KQSQHMTEV	1404	500	130	170	285	--	4	
p53.187	11	GLAPPQHILRV	1405	79	39	11	55	--	4	
p53.193	11	HLIRVEGNLRV	1406	385	1387	83	1194	1778	2	
p53.229	9	CTTIHYNM	1407	278	287	2564	561	181	3	
p53.263	10	NLLGRNSFEV	1408	217	--	2500	881	--	1	
p53.264	9	LLGRNSFEV	1409	85	358	37	206	--	4	

Table XXVII. Immunogenicity of A2 supermotif peptides

Source	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound	CTL Wild-type <sup>1</sup>	CTL Tumor
p53.135	CQLAKTCPV	1410	208	43	143	90	-- <sup>2</sup>	4	1/4	0/1

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity =10,000nM.

147

*g2d*  
*cdm*

Table XXVIII. Crossbinding of A2 supermotif analogs

Source	AA	Sequence	SEQ ID		A*0201		A*0202		A*0203		A*0206		A*6802		No. A2 Alleles Crossbound
			NO:		nM		nM		nM		nM		nM		
p53.69	8	AAPPVAPA	1411		5000		1536		1177		1233		4706		0
p53.69L2V8	8	ALPPVAPV	1412		217		7167		500		285		67		4
p53.101	11	KTYQGSYGFR	1413		1786		896		--		514		615		0
p53.101L2V1	11	KLYQGSYGFRV	1414		81		48		24		116		--		4
p53.129	9	ALNKMFCQL	1415		735		391		19		73		--		3
p53.129V9	9	ALNKMFCQV	1416		75		165		7.7		15		--		4
p53.129B7V9	9	ALNKMFBQV	1417		192		391		23		49		--		4
p53.129	10	ALNKMFCQLA	1418		1316		1075		71		4625		--		1
p53.129V10	10	ALNKMFCQLV	1419		217		287		71		7400		--		3
p53.132	9	KMFCQLAKT	1420		333		33		18		106		--		4
p53.132V9	9	KMFCQLAKV	1421		33		8.4		7.7		15		--		4
p53.132B4V9	9	KMFBQLAKV	1422		125		13		9.1		37		8889		4
p53.132L2V9	9	KLFCQLAKV	1423		98		3.6		3.4		10		1270		4
p53.135	9	CQLAKTCPV	1424		208		43		143		90		--		4
p53.135L2	9	CLLAKTCPV	1425		125		506		67		370		--		3
p53.135B1B7	9	BQLAKTBPV	1426		102		71		15		67		--		4
p53.135B1L2I	9	BLLAKTBPV	1427		46		119		7.7		64		--		4
p53.139	9	KTCPVQLWV	1428		725		606		217		15		--		2
p53.139L2	9	KLCPVQLWV	1429		122		239		29		23		--		4
p53.139L2B3	9	KLBPVQLWV	1430		46		29		19		31		--		4
p53.149	9	STPPPGTRV	1431		909		1162		1031		--		129		1
p53.149M2	9	SMPPPGTRV	1432		172		215		13		425		667		4
p53.149L2	9	SLPPPGTRV	1433		122		226		13		9250		140		4
p53.164	9	KQSQHMTEV	1434		500		130		170		285		--		4
p53.164L2	9	KLSQHMTEV	1435		122		94		35		46		--		4
p53.216	10	VVVPYEPPEV	1436		617		1870		455		1194		--		1
p53.216L2	10	VLVPYEPPEV	1437		89		391		71		2056		--		3
p53.236	11	YMCNSSCMGGM	1438		667		391		67		974		5333		2
p53.236L2M1	11	YLCNSSCMGGV	1439		22		13		3.6		18		1569		4
p53.255	11	ITLEDSSGNLL	1440		1563		1265		2857		507		6667		0
p53.255L2V1	11	ILLEDSSGNLV	1441		33		123		71		206		--		4

-- indicates binding affinity =10,000nM.

*Handwritten notes:*  
GAD...  
JWV

Table XXIX. Immunogenicity of A2 supermotif analogs

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound	CTL Peptide <sup>1</sup>	CTL Wild-type	CTL Tumor
p53.69	8	AAPPVAPA	1442	5000	1536	1177	1233	4706	0			
p53.69L2V8	8	ALPPVAPV	1443	217	7167	500	285	67	4	2/4	1/3	0/3
p53.129	9	ALNKMFCQL	1444	735	391	19	73	-- <sup>2</sup>	3			
p53.129V9	9	ALNKMFCQV	1445	75	165	7.7	15	--	4	0/1		
p53.129B7V9	9	ALNKMFBQV	1446	192	391	23	49	--	4	2/4	0/3	0/2
p53.132	9	KMFCQLAKT	1447	333	33	18	106	--	4			
p53.132V9	9	KMFCQLAKV	1448	33	8.4	7.7	15	--	4	1/3	0/2	0/2
p53.132B4V9	9	KMFBQLAKV	1449	125	13	9.1	37	8889	4	5/5	0/4	0/4
p53.132L2V9	9	KLFCQLAKV	1450	98	3.6	3.4	9.5	1270	4	2/3	1/3	0/3
p53.139	9	KTCPVQLWV	1451	725	606	217	15	--	2			
p53.139L2	9	KLCPVQLWV	1452	122	239	29	23	--	4	2/5	2/3	1/3
p53.139L2B3	9	KLBPVQLWV	1453	45	29	19	31	--	4	3/4	2/3	1/2
p53.149	9	STPPPGTRV	1454	909	1162	1031	--	129	1			
p53.149L2	9	SLPPPGTRV	1455	122	226	13	9250	140	4	2/3	1/3	0/3
p53.149M2	9	SMPPPGTRV	1456	172	215	13	425	667	4	2/4	2/4	2/4
p53.216	10	VVVPYEPPEV	1457	617	1870	455	1194	--	1			
p53.216L2	10	VLVPYEPPEV	1458	89	391	71	2056	--	3	1/1	1/1	
p53.255	11	ITLEDSSGNLL	1459	1563	1265	2857	507	6667	0			
p53.255L2V11	11	ILLEDSSGNLV	1460	33	123	71	206	--	4	1/3	0/3	0/2

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity = 10,000nM.

*add. 1*  
*add. 1*

**Table XXX. DR supertype primary binding**

Peptide	DR147 Algo Sum	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR147 Cross- binding
39.0307	2	GFRLGFLHSGTAKSV	1461	P53.108	3	5.4	89	3
39.0308	2	LNKMFCQLAKTCPVQ	1462	P53.130	20	804	167	3
39.0309	2	MGGMNRRPILTIITL	1463	P53.243	--	--	--	0
39.0310	2	RRPILTIITLEDSSG	1464	P53.248	5000	4500	--	0
39.0311	2	KRALPNNTSSSPQPK	1465	P53.305	--	--	--	0
39.0312	2	DGEYFTLQIRGRERF	1466	P53.324	125	--	--	1

-- indicates binding affinity =10,000nM.

*Handwritten:*  
4  
add  
column

Table XXXI. DR supertype cross-binding

Peptide	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR2w2 β1 nM	DR2w2 β2 nM	DR6w1 9 nM	DR5w1 1 nM	DR8w2 nM	DR147 Binding	Broad Binding (5/8)
39.0307	GFRLGFLHSGTAKSV	1467	p53.108	2.6	5.4	89	253	167	76	100	29	3	8
39.0308	LNKMFCQLAKTCPV	1468	p53.130	20	804	167	5688	541	365	2500	1531	3	5

-- indicates binding affinity = 10,000nM.



Table XXX. DR supertype primary binding

Peptide	DR147 Algo Sum	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR147 Cross- binding
39.0307	2	GFRLGFLHSGTAKSV	1461	P53.108	3	5.4	89	3
39.0308	2	LNKMFCQLAKTCPVQ	1462	P53.130	20	804	167	3
39.0309	2	MGGMNRRPILTIITL	1463	P53.243	--	--	--	0
39.0310	2	RRPILTIITLEDSSG	1464	P53.248	5000	4500	--	0
39.0311	2	KRALPNNTSSSPQPK	1465	P53.305	--	--	--	0
39.0312	2	DGEYFTLQIRGRERF	1466	P53.324	125	--	--	1

-- indicates binding affinity =10,000nM.

Table XXXIII. HTL candidate peptides

Peptide	Sequence	SEQ ID NO:	DR1 nM	DR4w 4 nM	DR7 nM	DR3 nM	DR2w 2 $\beta$ 1 nM	DR2w 2 $\beta$ 2 nM	DR6w 1 9 nM	DR5w 1 1 nM	DR8w 2 nM	DR14 7 Bindin g	Broad Binding (5/8)	DR 3 Binder
39.0307	GFRLGFLHSGTAKSV	1485p53.108	2.6	5.4	89	--	253	167	76	100	29	3	8	0
39.0308	LNKMFCQLAKTCPVQ	1486p53.130	20	804	167	--	5688	541	365	2500	1531	3	5	0

-- indicates binding affinity = 10,000nM.